

Fig. 2 A

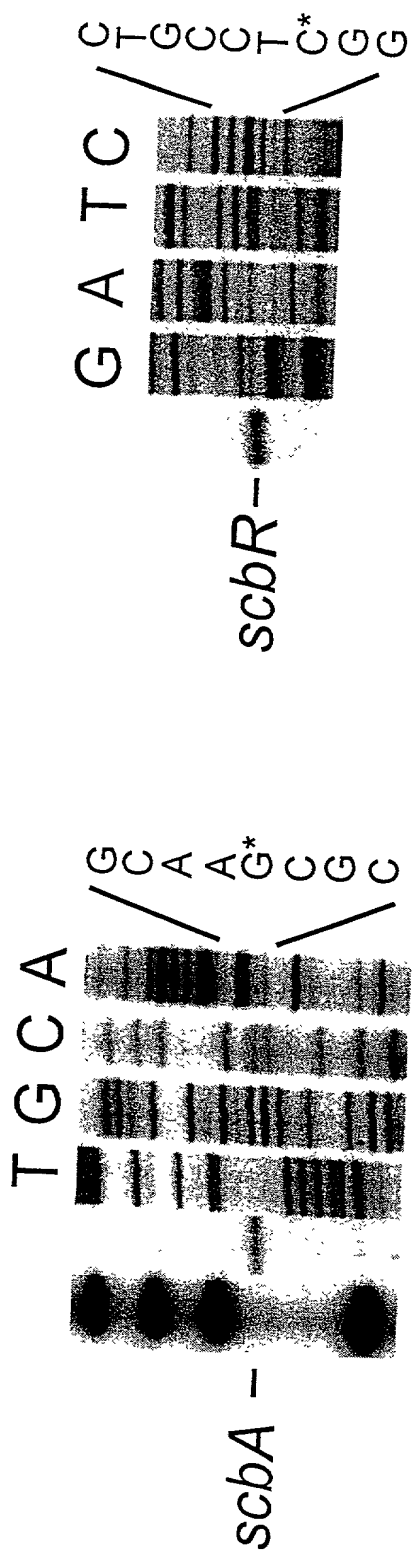


Fig. 2B

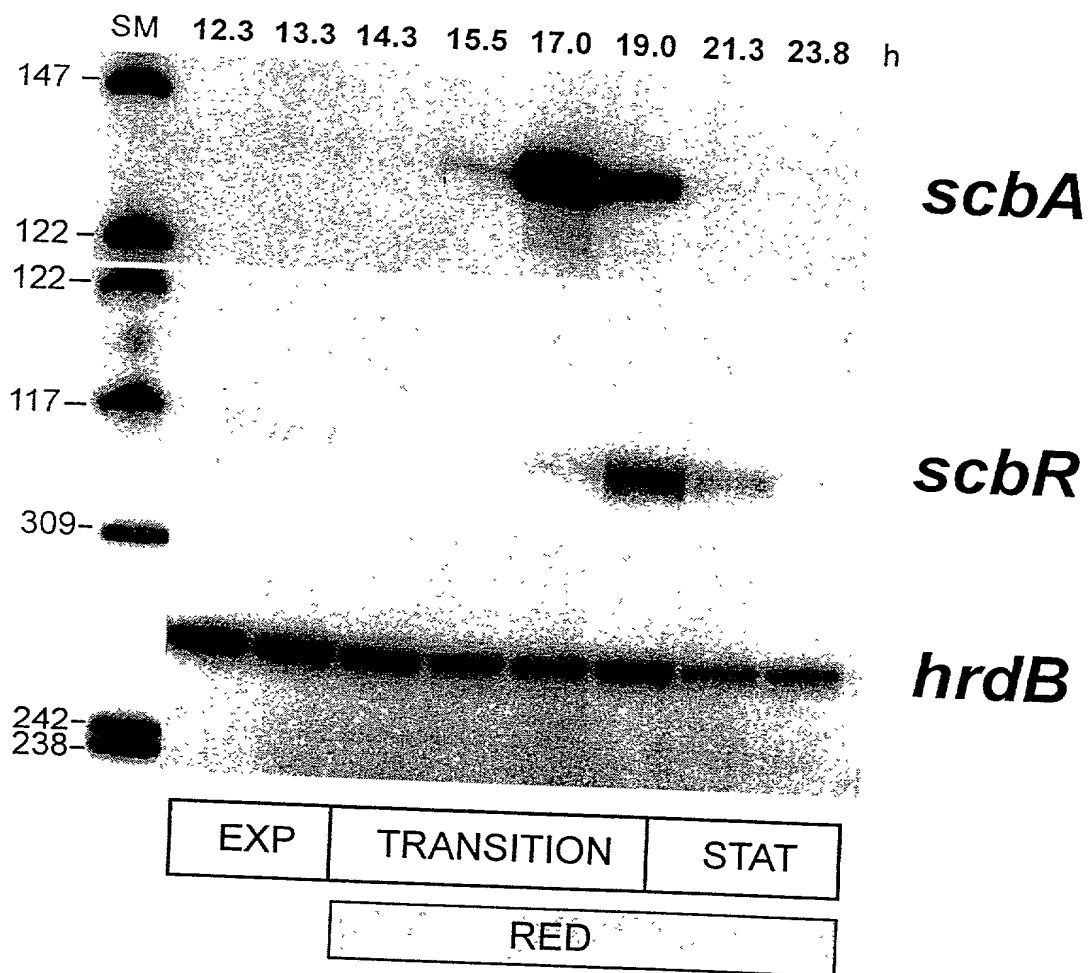


Fig. 3A

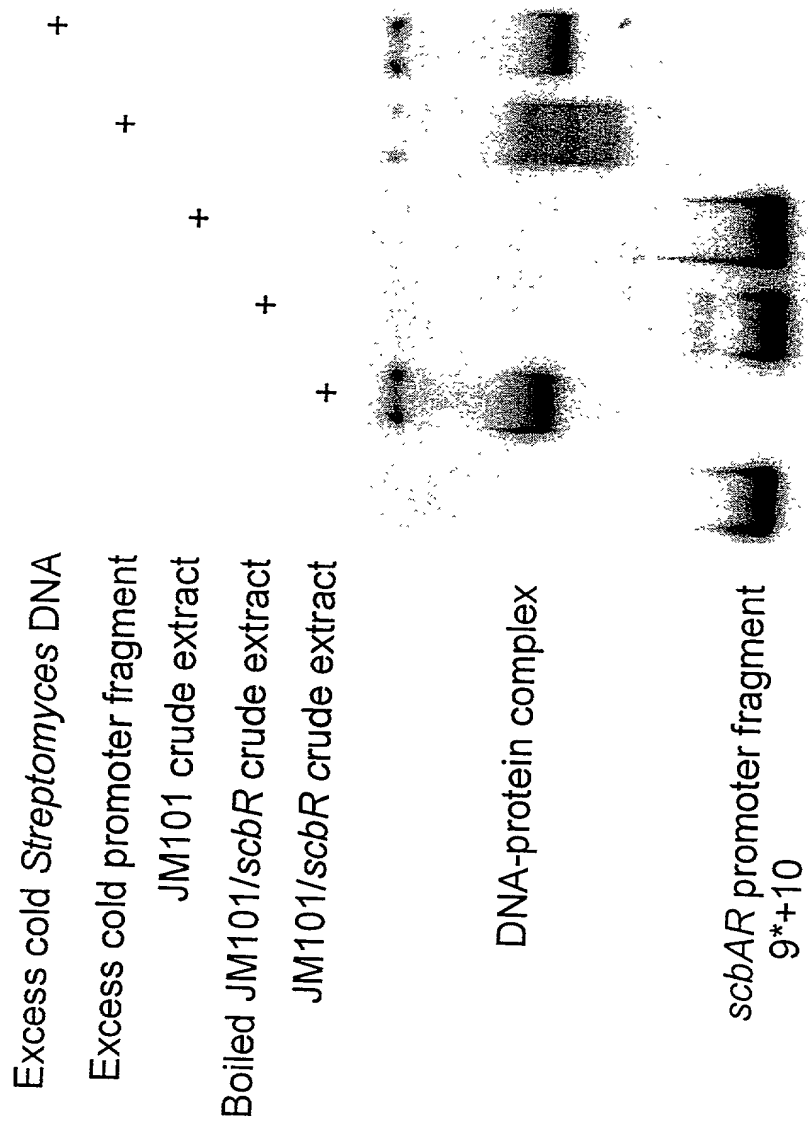


Fig. 3B

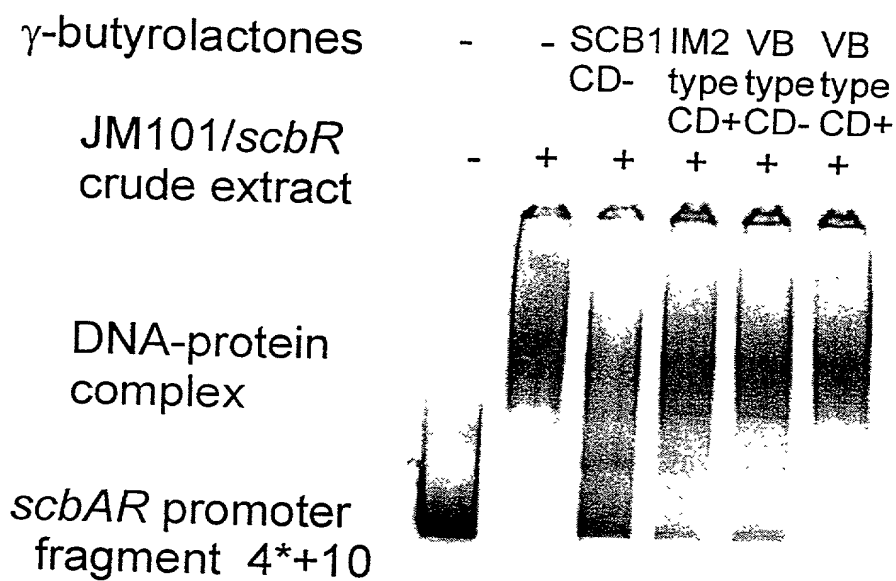


Fig. 4A

PCR fragment  
\*labelled oligo

9\*+10



9+10\*



JM101/*scbR*  
crude extract

— +

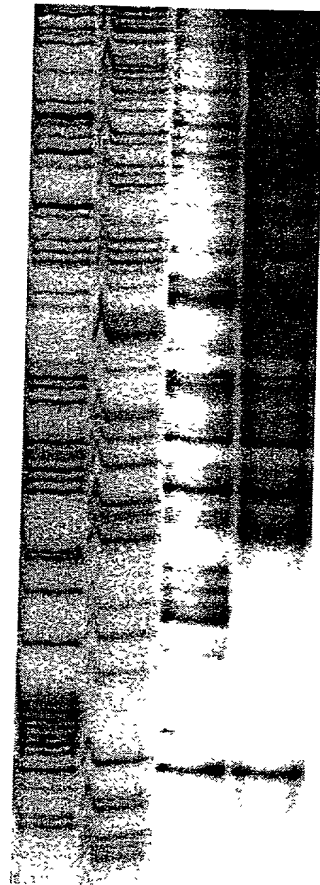
— +  $\nabla$

protein  
concentration ( $\mu$ l)

A G

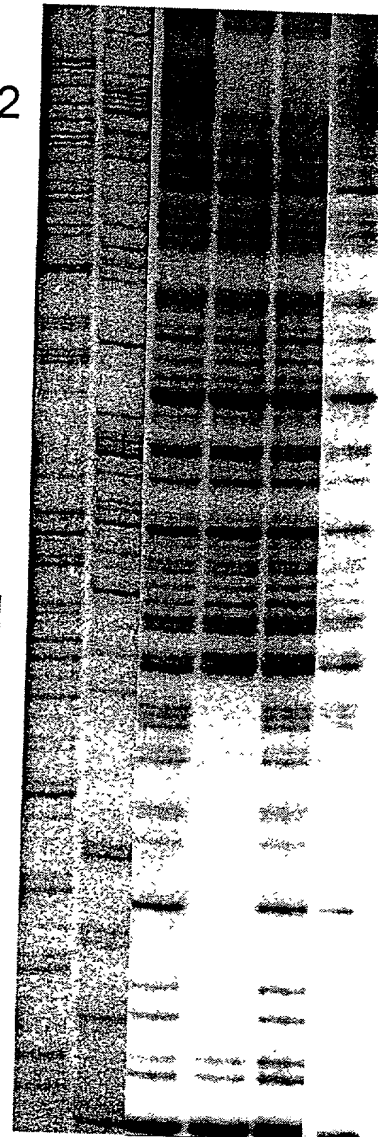
G A

2.5  
1.25  
0.16



No.2

No.1



No.1

No.2

fig. 48

sequence

```

GGGCAGGACGGCGGTGACCGAGAACCGGTCACCGCCCTTCGGTATCCAGCTGACCGGGAA
1  -----+-----+-----+-----+-----+-----+ 60
CCCGTCCTGCCGCACTGGCTCTTGGCCAGTGGCGGGAAGCCATAGGTCGACTGGCCCTT
  P L V A T V S F R D G G K P I W S V P F
                                -67 binding site No.2
CGCGTCCTGCACCCTGGTCCGGTGGACAAGCGCCATCGGAACCGGCAATGCGGTTTGTTT
61 -----+-----+-----+-----+-----+-----+ 120
GCGCAGGACGTGGGACCAGGCCACCTGTTGCGGGTAGCCTTGGCCGTTACGCCAAACAAG
  A D Q V R T R H V L A M P V P L A T Q E
                                +1 pscbR
                                ↗
-41
GATCGAGTTGGCATCGGACGCAGAATTGATCAAACTACTGCTTCGGGCATGGGTCCCCC
121 -----+-----+-----+-----+-----+-----+ 180
CTAGCTCAACCGTAGCCTGCGTCTTAAGTAGTTTTGATGACGAAGCCCGTACCCAGGGGG
  I S N A D S A S N I L V V A E P M [ScbA]
CCAGGAATCATGTGATGCCGAGCTGTTCTGTATGCGCGAACGTTAAGATACAGACTGAGC
181 -----+-----+-----+-----+-----+-----+ 240
GGTCCTTAGTACACTACGGCTCGACAAGACATACGCGCTTGCAATTCTATGTCTGACTCG
                                pscbA ← +1 -4 binding site No.1
GGTTTTTTTTTCTATCCTTCCCGGGGGAGACATGAACAAGGAGGCAGGCATGGCCAAGCAG
241 -----+-----+-----+-----+-----+-----+ 300
CCAAAAAAGATAGGAAGGGCCCCCTCTGTACTTGTTCCTCCGTCCGTACCGGTTGTC
                                -33 [ScbR] M A K Q
GACCGGGCGATCCGCACGCGGCAGACGATCCTGGACGCCGCGGCGCAGGTCTTCGAGAAG
301 -----+-----+-----+-----+-----+-----+ 360
CTGGCCCGCTAGGCGTGCGCCGTCTGCTAGGACCTGCGGCGCCGCGTCCAGAAGCTCTTC
  D R A I R T R Q T I L D A A A Q V F E K
CAGGGCTACCAAGCTGCCACGATCACGGAGATCCTCAAGGT
361 -----+-----+-----+-----+-----+ 401
GTCCCGATGGTTGACGGTGCTAGTGCCTCTAGGAGTTCCA
  Q G Y Q A A T I T E I L K

```

Fig. 5A

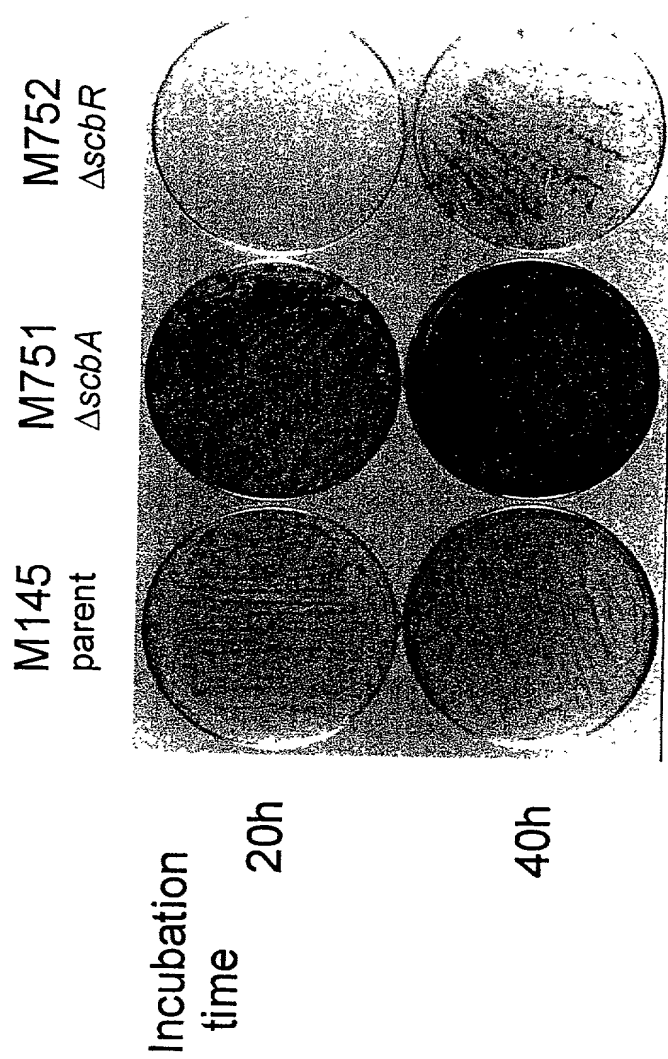




Fig. 58

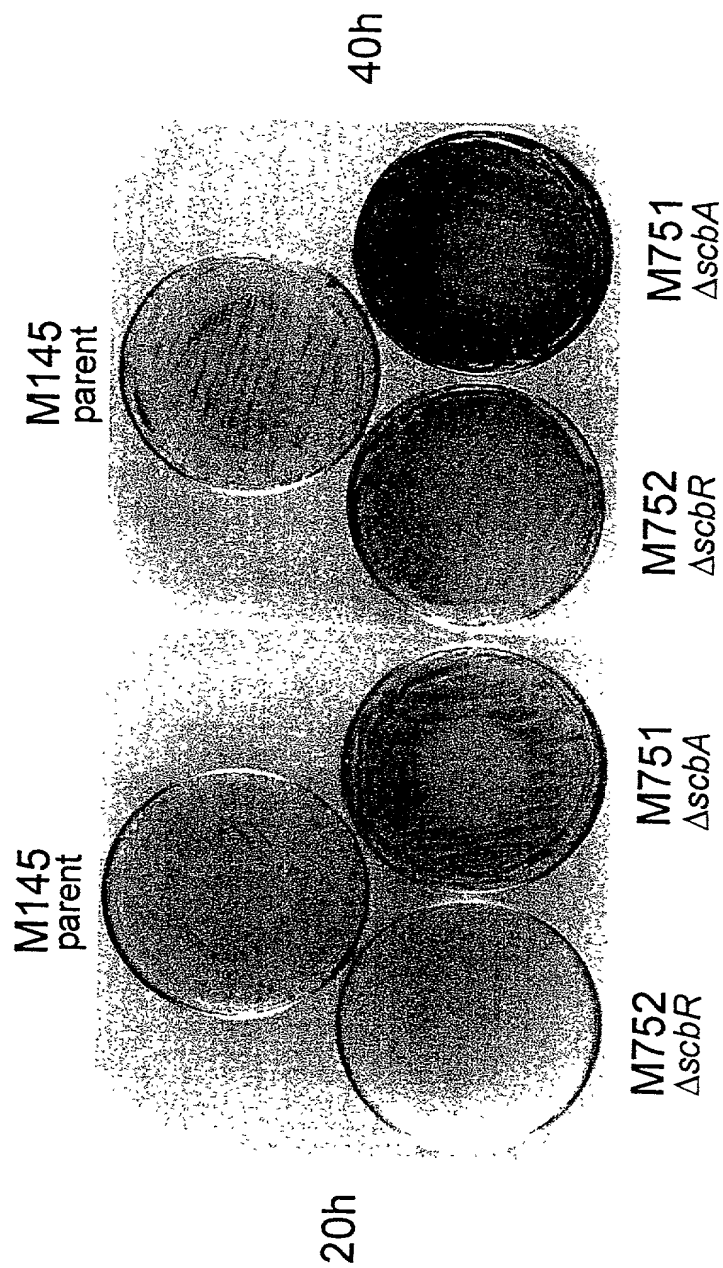


Fig. 6

M145(*pset152*)

M751(*pset152*)

M751(*scbA*)

M752(*pset152*)

M752(*scbR*)

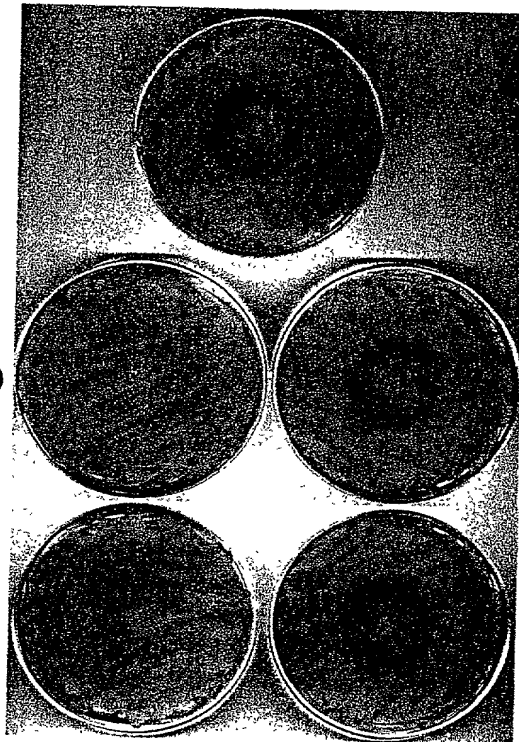


Fig. 7A

M145 M751 M752

1 2 3 4 5 6 1 2 3 4 5 6 1 2 3 4 5 6

*scbA*

*scbR*

*hrdB*

E	TRAN	S	E	TRAN	S	E	TRAN	S
---	------	---	---	------	---	---	------	---

RED

RED

A

Act production (ng/ml)	1) 12.0	3) 52	6) 200	1) 6.0	3) 250	6) 1844	1) 2.0	3) 6.0	6) 288
Red production (μg/ml)	1) 0.26	3) 0.44	6) 0.67	1) 0.06	3) 2.08	6) 6.40	1) 0	3) 0	6) 0.15

Fig. 7B

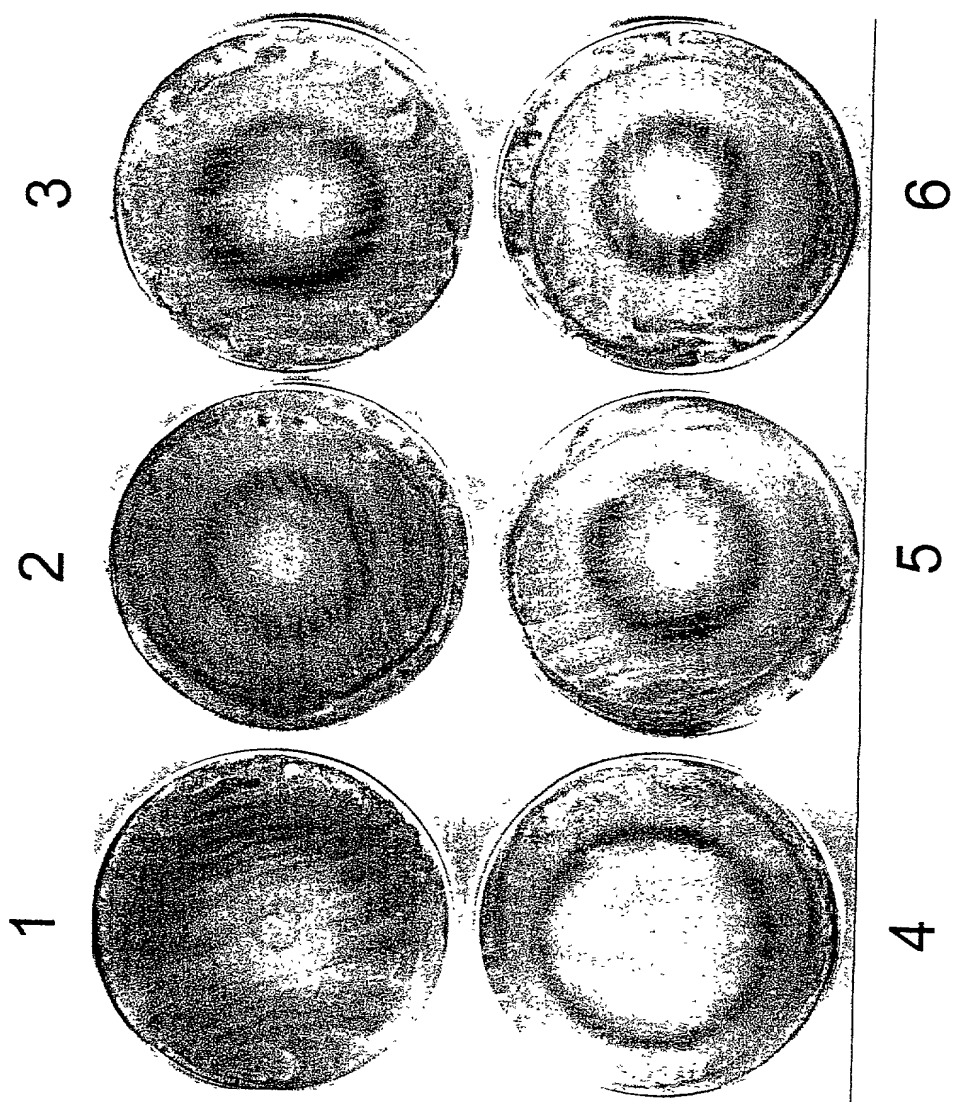


Fig. 8

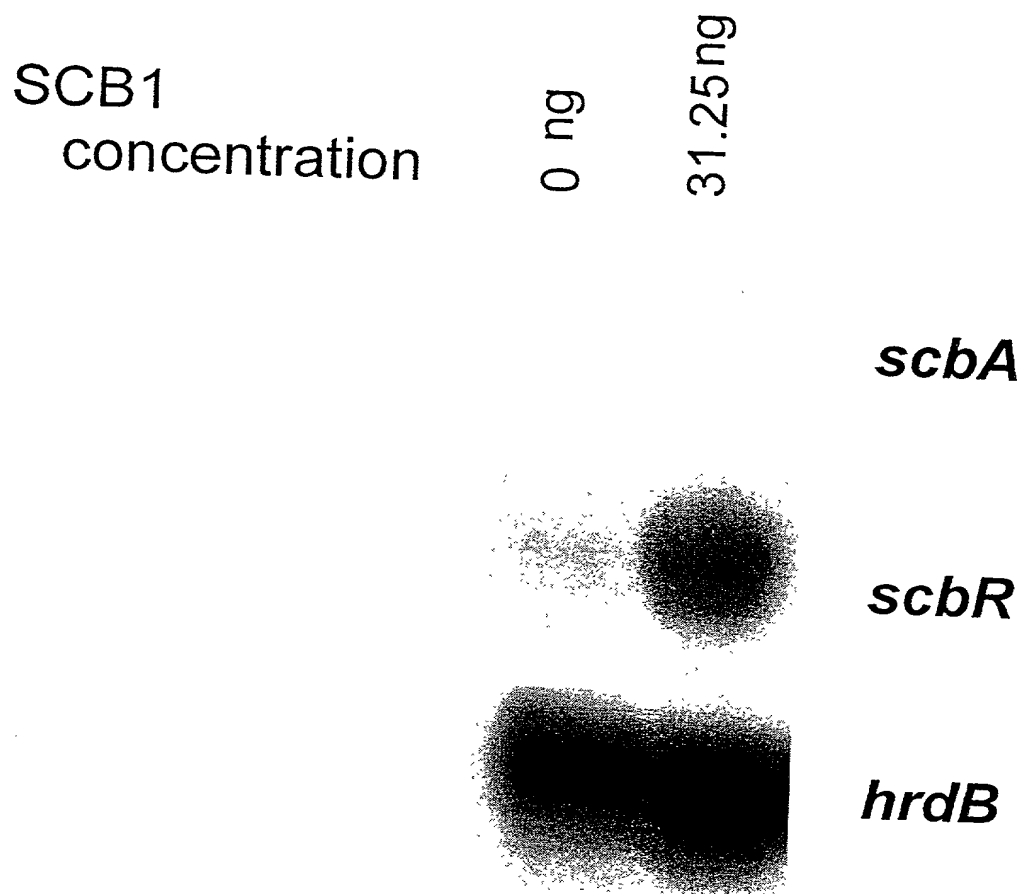


Fig. 9: ScbR amino acid sequence

MAKQDRAIRTRQTILDAAAQVFEEKQGYQAATITEILKVAGVTKG  
ALYFHFQSKEELALGVFDAQEPPQAVPEQPLRLQELIDMGMLFCHRLRTNVVARAGVR  
LSMDQQAHLDRRGPFRRWHETLLKLLNQAKENGELLPHVVTTDSADLYVGTFAGIQV  
VSQTVSDYQDLEHRYALLQKHILPAIAVPSVLAALDLSEERGARLAAELAPTGKD

Fig. 10: ScbA amino acid sequence

MPEAVVLINSASDANSIEQTALPVPMALVHRTRVQDAFPVSWIP  
KGGDRFSVTAVLPHDHPFFAPVHGDRHDPLLIAETLRQAAMLVVFHAGYGVVPVGYHFLM  
TLDYTCHLDHLGVSGEVAEEVEVACSQLKFRGGQPVQGQVDWAVRRAGRLAATGTA  
TTRFTSPQVYRRMRGDFATPTASVPGTAPVPAARAGRTRDEDVVLSSASSQQDTWRLRV  
DTSHPTLFQRPNDHVPGMLLLEAARQAACLVTGPAPFVPSIGGTRFVRYAEFDSPCWI  
QATVRPGPAAGLTTVRVTGHQDGSLVFLTTLSGPAFSG

Fig. 11: ScbB amino acid sequence

MRAHGTRYGRPLEGKTALVTGGSRGIGRGIALRLAADGALVAVH  
YGSSEAAAARETVETIRSSGGQALAIRAELGVVGDAALYAAFDAGMGEFGVPPEFDIL  
VNNAGVSGSGRITEVTEEVFDRLVAVNVRAPLFLVQHGLKRLRDGGRIINISSAATTR  
AFPESIGYAMTKGAVDTLTLALARQLGERGITVNAVAPGFVETDMNARRRQTPEAAAA  
LAAYSVFNRIGRPDDIADVVAFLASDDSRWITGQYVDATGGTIL

Fig. 12

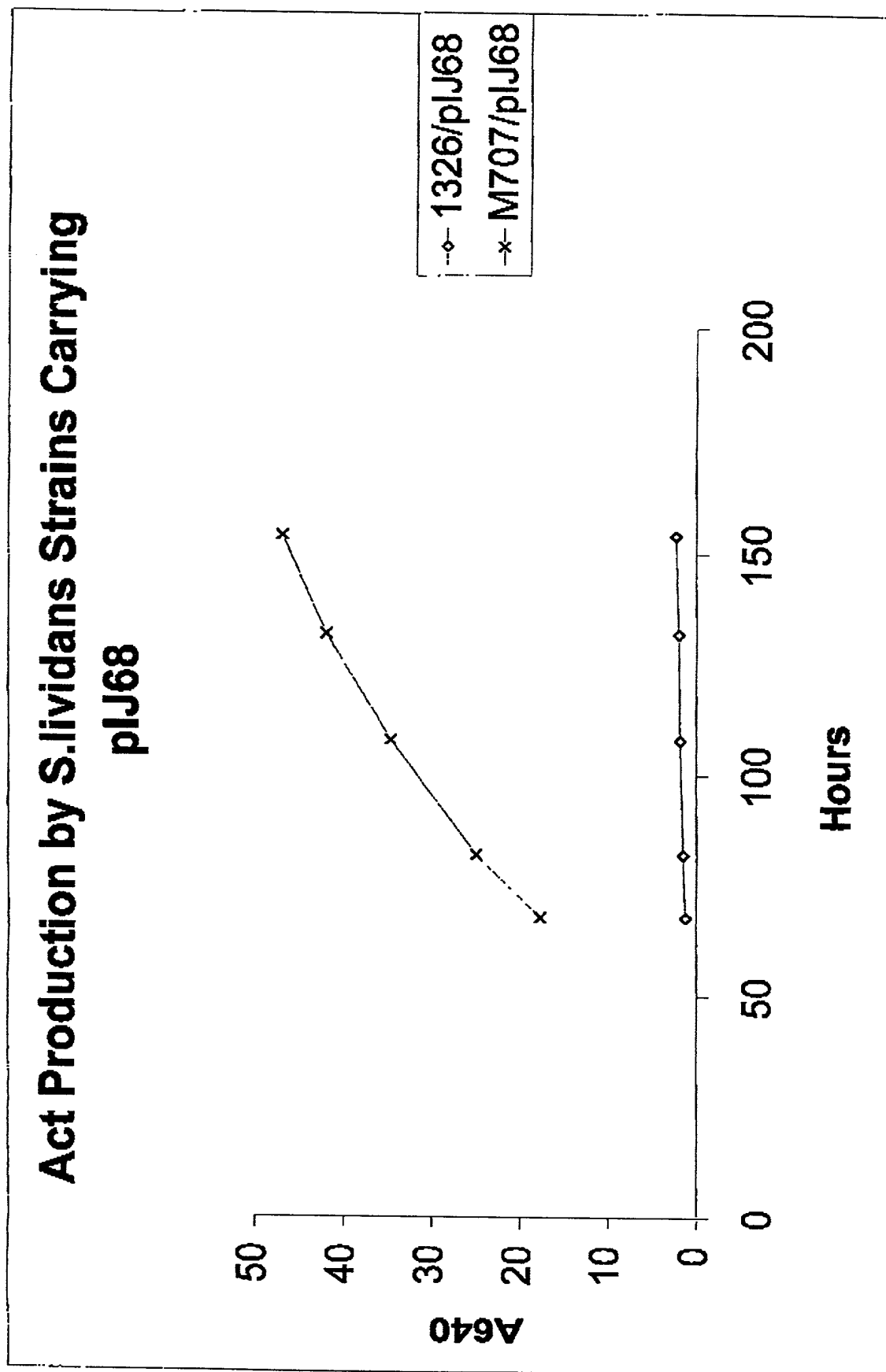


Fig. 13

# Red Production by *S. lividans* Strains Carrying pIJ6014

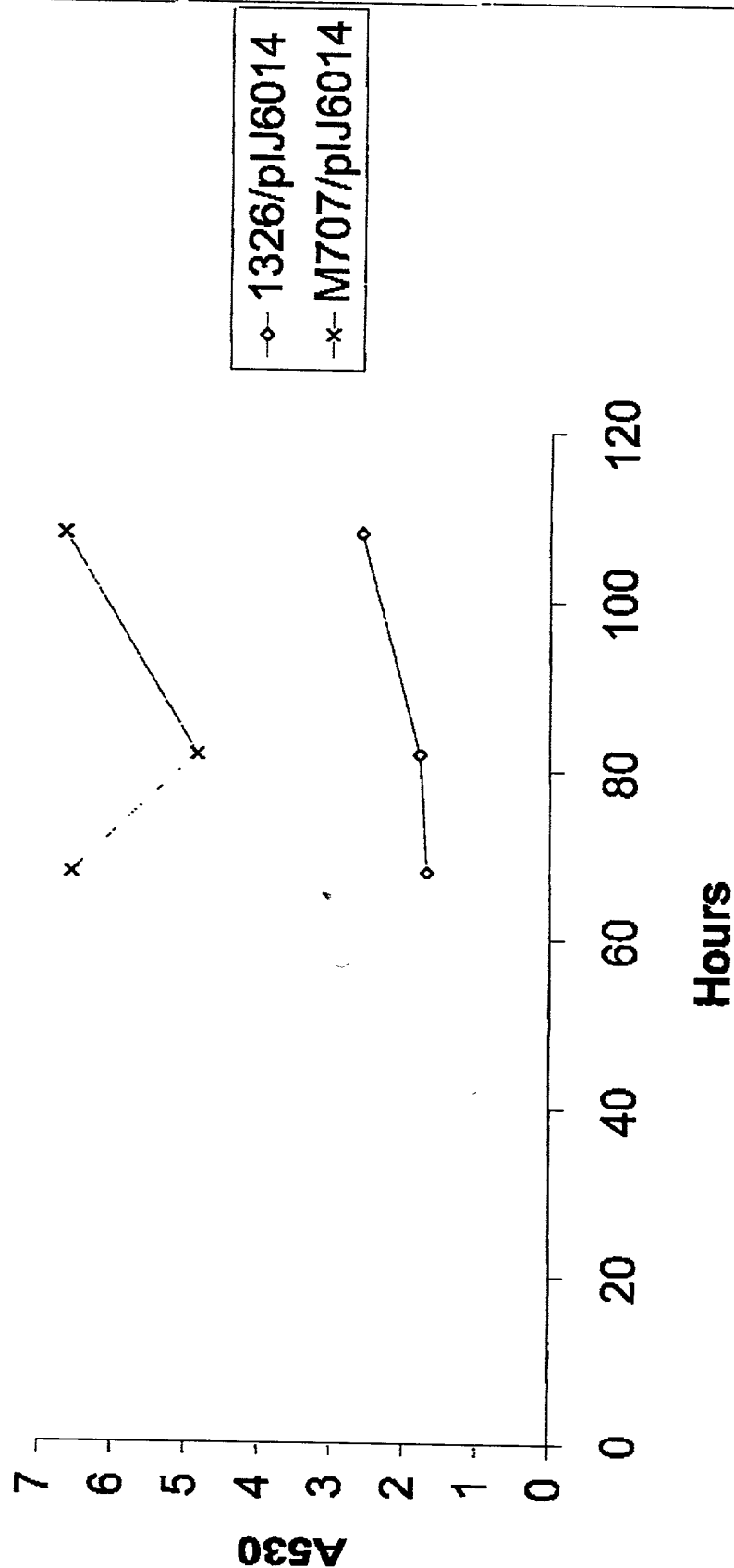




Fig. 14

DNA\_SEQUENCE Length: 4346kb..

1 **GTCGACGACG** GCGTCGGGTT CGACGCCGAC GCGGTACTCG TTCCCGGCCA  
*HincII*

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101 GCGGCTCCT GATAGTGAGC GGCCCCGCCG GCGGCACGCA CATCGACGTC  
151 CATCTCCCAC TGCGCCCCCG GAAAGTGAGC ACCGCACCGC GGACGTGACG  
201 CCATGGGAGG GCCACGTCCG CGGACGGATC ACCCCTGGCT TCGGCCGAAG  
251 GCTTCCGCGT GGTCCGCCGC CCAGATGCGG AACGGCCTGG CGGGCCGGCC  
301 CGTCACTTCC CGCACGGTCG GCACGACCTG CGCCTTGGCC CCCGCCCGCT  
351 GCCGCTCGGC GCTCTCCAGG AACGCGTCGG CGACGGGCCT CGGATACTTC  
401 CGGAGCATCT GCTCGCGCGC CGCCTCCAGC CCCAGCTCCT CGAAACGCAG  
451 TGACCGCCCC AGCACCTCGG AGAGCCGCGC CGTCTGCTGC CTGGCGGTGA  
501 TCGCCTCGGG CCCGGACAGC GCGTACGCCC GTCCCTCGTG GCCGGGCCGG  
551 GTCAGTGCCC TGACCGCCAC TTCCGCGATG TCGCGCGGAT CGACGCAGGC  
601 AACCAGGGGAC GTGCCGTACA GCGCGCGGAC CACGCCGTCG GACCGGATGG  
651 CGGGCGCCCA GGACAGCGTG TTGGACATGA AGGTCCTGGC CCGCAGGAAG  
701 GTCCAGTCTA GCCC GGACTC GCGTACGGCC CGCTCGTTCT CGCGCTGCCG  
751 CCGCGTGATG AAGTCGTCCG CGCCCGGTTT CCCCACCGCG AGCATGGACA  
801 GCTTCACCAG GTGCCGGACG CCGGCCTCGC GCGCCGCCGC CGCGAAACGC  
851 TCGTCGTCCG GCTCGGTGGC ACTGTTCGTG ACGAGGAACG CCGCCCGCAC  
901 CCCGTTGAGG GCCC GGTTCCA GGCCCGGGCG GTCGGCGTAC TCGCCCGCGC  
951 AGACCTCGAC GTTCGGGCCG GTGACGGTCA CCCGTTCCGG CCGCCGGGCG  
1001 AGGACTCTGA CGGGACCGGT CCGGGCCAGC AGGTGGGCGA CCTGACGGCC  
1051 GACCACACCG GTCACGCCGG TCACAAGAAT CACTCGGGGC TCCTCTCGGG  
1101 CAGCGAGGCA GGGGCGCCTC CGaacAtACA TATGAGGGGA Agggcaggat  
1151 ctgccccggg gcgcgaaccg gcgatgttcg cgccccGGGG CCGGTGCTTC  
1201 AGCCGGAGAA CGCGGGGCCG GACAGCGTGG TGAGGAAGAC GAGGCTGCCG  
1251 TCCTGATGCC CCGGTGACCCG CACGGTGGTC AGCCCCGCCG CCGGCCCGG  
1301 CCGGACCGTC GCCT**GGATC/C** AGCACGGGCT GTCGAACTCC GCGTACCGGA  
*BamHI*

1351 CGAACCGGGT GCCGCCGATC GACGGCACGA AGGGCGCCGG ACCGGTCACG  
 1401 AGGCACGCCG CCTGCCGTGC CGCCTCGAGC AGCAGCATGC CCGGTACGTG  
 1451 GTCGTTGGGG CGCTGGAAGA GGGTCGGGTG ACTGGTGTCC ACCCGCAGTC  
 1501 GCCACGTGTC CTGCTGCGAA CTCGCCGACA GGACCACGTC CTCGTCGCGG  
 1551 GTGCGACCGG CGCGCGCCGC GGGCACGGGC GCGGTCCCGG GCACCGATGC  
 1601 GGTGGGAGTC GCGAAGTCGC CGCGCATCCG CCGGTAGACT TGAGGACTGG  
 1651 TGAAGCGCGT CGTGGCAGTC CCCGTGGCAG CGAGCCGTCC GGCGCGGCGC  
 1701 ACGGCCAGT CCACCTGTCC CTGTACGGGC TGCCCGCCGC GGAACCTCAG  
 1751 CTGGGAACAG GCCACTTCCA CCTCCAGCTC CGCGACCTCG CCCGACACGC  
 1801 CGAGGTGGTC GAGGTGGCAG GTGTAGTCCA GCGTGGCCAT CAGGAAGTGG  
 1851 TAGCCCACCG GCACGCCGTA GCCGGCGTGG AAGACGAGCA TCGCCGCCTG  
 1901 ACGCAGGGTC TCGGCGATCA GCAGCGGATC GTGTCGGTCC CCGTGGACCG  
 1951 GTGCGAAGAA CGGGTGGTCG TGGGGCAGGA CGGCGGTGAC CGAGAACCGG  
 2001 TCACCGCCCT TCGGTATCCA **G/CTG**ACCGGG AACGCGTCCT GCACCCTGGT

*PvuII*

2051 CCGGTGGACA AGCGCCATCG GAACCGGCAA TGCGGTTTGT TCGATCGAGT  
 2101 TGGCATCGGA CGCAGAAATTG ATCAAACTA CTGCTTCGGG CATGGGTCCC  
 2151 CCCCAGGAAT CATGTGATGC CGAGCTGTTC TGTATGCGCG AACGTTAAGA  
 2201 TACAGACTGA GCGGTTTTTT TTCTATCCTT CCCGGGGGAG ACATGAACAA  
 2251 GGAGGCAGGC ATGGCCAAGC AGGACCGGGC GATCCGCACG CGGCAGACGA  
 2301 TCCTGGACGC CGCGGCGCAG GTCTTCGAGA AGCAGGGCTA CCAAGCTGCC  
 2351 ACGATCACG/G AGATCCTCAA GGTGGCCGGG GTGACCAAGG GAGCCCTCTA

**CTGCA/GATG** designed primer to generate *PstI* site

*PstI*

2401 CTTCCACTTC CAGTCCAAGG AAGAACTGGC GCTGGGCGTC TTCGACGCCC  
 2451 AGGAACCACC ACAGGCCGTT CCGGAGCAAC CCCTCCGGCT GCAAGAACTC  
 2501 ATCGACATGG GCATGTTGTT CTGTCACCGC TTGCGCACGA ACGTCGTGGC  
 2551 CCGGGCCGGC GTGCGCCTCT CCATGGACCA GCAGGCGCAC GGTCTCGATC  
 2601 GCCGAGGACC CTTCCGTCGC TGGCACGAGA CACTCCTGAA GCTGCTGAAC  
 2651 CAGGCCAAGG AGAACGGTGA GTTGCTGCCC CATGTGGTCA CCACCGACTC  
 2701 GGCCGATCTC TACGTGGGCA CGTTCGCCGG GATACAGGTC GTGTCCAGCA  
 2751 CGGTCAGCGA CTACCAGGAC CTCGAACACC GCTACGCGCT **GCTGCA/GAAG**

*PstI*

2801 CACATCCTGC CCGCCATCGC GGTTCCTCC GTGCTGGCCG CGCTCGATCT  
 2851 CTCCGAGGAG CGCGGAGCAC GCCTCGCGGC CGAACTGGCA CCGACCGGGA  
 2901 AGGACTGACC GCCGAAGCGC CCGCACC GGA TACCGACCCG CCGTGCCCGA  
 2951 GCGGCCGACC GGGGCCGCCT ACGGGCCCGG CGGCGGGCCC GTAGGTCTGC  
 3001 CCTGCGTACC GAAGCGTGCG GGGTCAGAGA ATCGTTCCGC CTGTGGCATC  
 3051 GACGTACTGG CCGGTGATCC ACCGTGAGTC GTCGGAGGCC AGAAAGGCCA  
 3101 CCACGTCGGC GATGTCGTCG GGTCTGCCGA TCGGGTTGAA CACGGAGTTG  
 3151 GCGGCCAGTG CCGCGGCCGC CTCGGGGGTC TGCCGCCGCC GTGCGTTCAT  
 3201 GTCCGTCTCC ACGAAACCCG GCGCCACCGC GTTGACCGTG ATCCCCCGTT  
 3251 CCCCCAGTTG CCTGGCCAGG GCGAGCGTGA GCGTGTCCAC CGCACCCCTG  
 3301 GTCATCGCGT ATCCGATGGA CTCGGGGAAC GCGCGCCGGG TCGCGGCAGA  
 3351 CGAGATGTTG ATGATCCGCC CGCCGTCGCG CAGTCGTTTC AGTCCGTGCT  
 3401 GGACCAGGAA CAGCGGTGCC CGGAC**GTGA** CGGCGACCAG TCGGTCGAAG

*HincII*

3451 ACCTCCTCGG TGAATTCCGT GATCCGTCCC GAGCCGCTGA CGCCCGCGTT  
 3501 GTTCACCAGG ATGTCGAACT CGGGCGGCAC TCCGAACTCG CCCATCCCGG  
 3551 CGTCGAACGC CGCGTAGAGC GCGGCCGCGT CACCCACGAC GCCGAGTTCTG  
 3601 GCCCGGATGG CCAACGCCTG TCCGCCGCTG CTCCGGATGG TCTCGACGGT  
 3651 CTCTCGCGCC GCCGCCTCGC TGCTGCCGTA GTGGACTGCC ACGAGCGCCC  
 3701 CGTCCGCGGC CAGCCGCAGG GCGATACCGC GTCCGATGCC CCGGCTTCCC  
 3751 CCGGTCACCA GGGCGGTCTT GCCCTCCAGC GGTCTTCCAT ACCTCGTCCC  
 3801 ATGTGCACGC ATATCAGCCC CCGCCGTGCG TGAGCGACCC ATGGCGGCCG  
 3851 CTCGGCCGTT CGAATCGACG GTCACAGCCT ACCTGTGACC GCGTCAGACG  
 3901 GGGCCGGAGT GGCCCGGTTG GACGGCTGGG GCCAGATCGG GCGGCGCGCA  
 3951 CGGGGAACCG GCGCCGGTCA GGGGTCAGGG GTCGCCGGGA CCGCCAGGC  
 4001 CGGTACAGGC ACCGACCGGA TCGAGGTCGG GCGTGCCACG CGGCCACCAG  
 4051 TCCTCGCGGC CCAGCTCCGA CTCGTACGCG TACCAGAGCC CGGTCCGGCC  
 4101 GAGTCTGAGC TGGACGTGGC CGCGCGGGTG GGTGAGGCGG TTGCGCCAGG  
 4151 GGCGGAAGGC GGGGAGGTCG GCGGCGAGCA TCATGGGGCG GGCGCGGTCTG  
 4201 AAACGGCCGG CCGGCGGGTC CCAGGGCTCC TCCAGGACGT CTAGACCCGC  
 4251 CAACCCGCCC TGCCGCCAGG CGGCGACGGC CCGCGCCAGC TCCGCCGTGT  
 4301 CGCGTCCGGC GGCCGAGGCG AGCGACGCGT AGAGCGCGCG **GGTACC**

*KpnI*